

QY 701 ProProAlaGlnProProGlyProProAsnAlaSerSerAnProAspLeuArgArgSer 720
 Db 2086 -----AGTAACCCCGACCTCCAGAGAGAGC 2109
 QY 721 AspProGlyTTPGluArgSerAspSerValLeuProAlaSerHisGlyHisLeuProGln 740
 Db 2110 GACCCCTGGCTGGAGACGCTCGACAGGTCCTTCAGCCCTCAGCGGACCTCCCCAG 2169
 QY 741 AlaGlySerLeuGluArgAsnArgValGlyVala-SerSerLeuLeu-AspSerSerProV 760
 Db 2170 GCTGGCTCACTGGAGCGGAACCCGCTGGAGT-CTCCTCCAAAC-C-GACAGCTCCCTG 2227
 QY 760 allLeuSerProGlyAsnValAlaValProAspAspHisArgSerArgProGlyArgPro 780
 Db 2228 TGCTTCCTCCCTGGAAATAAGCCAGCCGACCAACCCGCTACCGGCGGCGGCGCCG 2287
 QY 780 laAspPheValLeuLeuValArgThrLeuAspGluAlaProArgProProGlyVala 800
 Db 2288 CAGACTTGTGTGCTGGAAGAGCGACTCTGACAGGCCCTCCGCTCCCAAGAGG 2347
 QY 800 laMetAspTyrSerSerSerSerGluGluValaGluSerSerGluAspAspGluGluGlu 820
 Db 2348 CCATGCACTACTGCTGCTCAGCGAGAGAGGTGGAAGAGTGAAGCAGACGAGAGAGAG 2407
 QY 820 lylGluGlyValProAlaGluGlySerArgAspThrProGlyValArgSerAspGlyVal 840
 Db 2408 GCGAAGCGCGCGCAGAGAGAGAGAGAGATACCCCTGGGGCGCCAGAGAGAGAGATA 2467
 QY 840 hrAspSerValSerThrMetValaHisAspValGluGluLeuThrGlyThrGlnPro 860
 Db 2468 CAGACGCGCTCAGACCACTGTGTCTCAGACTCAGAGAGATCAGCGGAGCCAGCCG 2527
 QY 860 rorTylGlyGlyThrMetValaGlnArgThrProGluGluGluArgAsnLeuLeu 880
 Db 2528 CATACGGGGCGGCACTAGTGTGTCTCAGCGCACCCCTGAAGAGAGAGAGAGAGAG 2587
 QY 880 laAlaAspSerArgGlyTyrThrAsnLeuProAspValValGlnProSerHisSerPro 900
 Db 2588 ATGTCTACAGCAATGGGTACCAAACTCTGTCAGTGTGTCCAGCCAGCACTCAGCCA 2647
 QY 900 hrGluAsnSerLysGlyGlnSerProProSerLysAspGlySerGlyAspTyrGlnSer 920
 Db 2648 CCGAAGACGCAAGAGCCAAAGCCCACTCAGAGAGAGAGAGAGAGAGAGAGAGAG 2707
 QY 920 rgglyLeuValaLysAlaProGlyLysSerSerPheThrMetPheValaAspLeuGlyLeu 940
 Db 2708 GTGGGCTGGTAAAGCCCTGGGCAAGAGTCTGTCAGATGTTGTGATCTAGGATCT 2767
 QY 940 yrgLInProGlyLysSerGlyAspSerLysProLysLeuValaGlyGlyGluGlyT 960
 Db 2768 ACCAGCTCTGAGAGCAAGTGGGAGAGATCCCTCAGAGAGAGAGAGAGAGAGAG 2827
 QY 960 hrArgLeuAspGlnLeuGlnTyrAspValArgLysGlySerValaAsnValaAsnPro 980
 Db 2828 CTCGGCTCAGACGCTCGACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2887
 QY 980 hrAsnThrArgLysHisSerGluThrProGluLysArgLysTyrLysValArgPheAsn 1000
 Db 2888 CCAACACCCCGGCGCAGATGAGACCCCTGAGATCCGGAAGTACAGAGAGAGAGAG 2947
 QY 1000 erGluLysLeuGlyAlaAlaLeuTyrGlyValaAsnLeuValaGlyThrGluAsnGly 1020
 Db 2948 CCGAGATCTCTGTGAG 3007
 QY 1020 euMetLeuAspArgSerGlyGluGlyValaValaTyrGlyLeuLeuGlyArgArgArg 1040
 Db 3008 TGAATGTCTGAGACCAAGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3067
 QY 1040 heGlnGluMetAspValLeuGluGlyLysAsnLeuLeuLeuThrLysSerGlyLysArg 1060
 Db 3068 TCACAGAGATGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3127

QY 1060 snLysLeuArgValTyrTyrLeuSerTyrPheArgAsnLysIleLeuHisAsnAspPro 1080
 Db 3128 ACAAACCTGGGGTGTATTAACCTGTCTGTCTGCGGAGACAGATTCAGACATAGCCAG 3187
 QY 1080 luValGluLysLysGluGlyTyrThrThrValaGlyAspMetGluGlyCySGlyHisTyr 1100
 Db 3188 AAGTGAAG 3247
 QY 1100 rgyValValaLysTyrGluValaGlyLysPheLeuValaIleAlaLeuLysSerSerValaGlu 1120
 Db 3248 GTGTGTGTGAATACAGAGCGAGATTAAGTTCCTGTCTCCTCCTCAGAGACTCCGTGAGAG 3307
 QY 1120 alTyrAlaThrPheLysProLysProLysPheLysPheMetAlaPheLysSerPheAlaAsp 1140
 Db 3308 TGTATGCTGGGCGCCCAACCCCTACCAAAATTCATGAGCTTCAGAGCTTCCTGCGAGCC 3367
 QY 1140 euProHisArgProLeuLeuValaAspLeuThrValaGluGluGluGluValaIle 1160
 Db 3368 TCCCCACCGCCCTCTGTGTGTGACCTGACAGTGAAGAGAGAGAGAGAGAGAGAGAG 3427
 QY 1160 leryTylSerSerAlaGlyPheHisAlaValaAspValaAspSerGlyAsnSerTyrAsp 1180
 Db 3428 TCTATGCTCTCAGAGTGTGTCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3487
 QY 1180 leryTylLeuProValaHisIleGlnSerGlnIleThrProHisAlaIleIlePheLeuPro 1200
 Db 3488 TCTACATCTCTGTGACATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3547
 QY 1200 snThrAspGlyMetGluMetLeuLeuCyTyrGluAspGlyValaTyrValaAsnThr 1220
 Db 3548 ACACGAG 3607
 QY 1220 yrglyValaGlyLysAspValaValaLeuGlnTyrGlyGluMetProThrSerValaIle 1240
 Db 3608 ACGGCGCATCATTAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3667
 QY 1240 yrlleCySerSerArgGlnIleMetGlyTyrGlyGluLysValaIleGluLysSerVala 1260
 Db 3668 ACATCTGTCTCACAAGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3727
 QY 1260 luThrGlyHisLeuAspGlyValaPheMetHisLysArgAlaGlnArgLeuLysPheLeu 1280
 Db 3728 AAGCGGCGCATCTCAG 3787
 QY 1280 ysgLysAspAspLysValaPhePheAlaSerValaArgSerGlyLysSerGlnVala 1300
 Db 3788 GTGAGGAGATGATCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3847
 QY 1300 yrfPheMetThrLeuAsnArgAsnCyGlyMetAsnTyr 1312
 Db 3848 ACTTCATGACTCTGAACCGTATCATCATCATCATCATCATCATCATCATCATCATCAT 3885
 RESULT 2
 AB035698/c
 / TOIG OF: ab035698 check: 9874 from: 1 to: 3888
 /
 / LOCUS AB035698 3888 bp mRNA linear PRI 18-APR-2000
 / DEFINITION Homo sapiens mRNA for Mieshaen/NIK-related kinase MINK-1, complete
 / cde.
 / ACCESSION AB035698
 / VERSION AB035698.1 GI:6970477
 / KEYWORDS
 / SOURCE Homo sapiens (human)
 / ORGANISM Homo sapiens
 / Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 / Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 / 1 (sites)
 / REFERENCE Dan,T., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
 / Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
 / Matsumoto,K., Niimiya-Tsuji,J., and Kusumi,A.
 / Molecular cloning of MINK, a novel member of mammalian GCK family
 / kinases, which is up-regulated during postnatal mouse cerebral
 / development.

[illegible]

OY	25	e-GluLeuValGluValValGlyAsn-Gly-----ThrTrgYly-----G1	38
Db	3661	CAGAGTC-AT-GAGGTA-----AACTTGCTGCTGCCCCCAGAGC---GGACTGAGCA	3813
OY	38	n-----Val-TyrLysGlyArg-HisValLysThrGlyGlnLeu-Ala-----A1	52
Db	3812	AAAAACACCTGTGATTC-----CGCTCAC-----ACAGGAGC-CTGAGCCTTGAGC	3766
OY	52	a-IleLysVal-Met-Asp---ValThrGluAspGluGluGlnIle---LysGlnG	69
Db	3765	TCGTTT--GTGCATGAAGACCCCTTC-----GAGGTGACCGGT-----	3730
OY	69	IuIleAsnMetLeuLysLysTyrSerHisHisGlyAsn-IleAlaThrTyrTrgYlyA1	88
Db	3729	-----CTC-----CACAGAGC-GGATC---TCAAI---GGCT-3705	
OY	88	apheIleLysLysSerProProGlyAsnAspAspGln--Leu--TrpLeuValMetG1	106
Db	3704	---TTC-----TCACCC-----CAGCCCATATTCGGTTG-----GA	3676
OY	106	uPhe--Cys-GlyAlaGlySerValThrAspLeuValLysAsnThrLysGly-----	122
Db	3675	GCA-GATGTAGGCC-----ACAGAA--GTA-----GGCATCTCCCC	3643
OY	123	Asn-----Ala-----LeuLysGluAsp--CysIleAla--TyrIleCys--ArgG1	136
Db	3642	CCACTGCAGCACCAATCTT-----AAATGATGC--GCCGTAGC--TGTGACGT--	3596
OY	136	uIleLeuArgG1LysuAlaHis-----Leu--His-Ala-HisLysValIleHis-	151
Db	3595	-----AGA-----CACCTGCTCCTCGAGCAGCAGCAGCAT-----CTCATG	3558
OY	152	ArgAspIleLysGlyGlnAsnValIleLeuThrGlnuAlaGluValLysLeuValAs	171
Db	3557	CCGTCG-----GTG--TTGGG-GAG-----GAA-----GA	3536
OY	171	pPhe-----GlyVal-Ser-AlaGlnLeuAspArgThrValGlyArgArgAsnThr	188
Db	3535	TGA-TGCAGTGGGGCGGTGATCTGACT--CTGGAT-----GTGC-----ACA	3498
OY	188	heIleGlyThrProTyrTrpMetLarProGluValIleAlaCysAspGluAsnProAspA	208
Db	3497	-----GGG-----ATG--A--GATGCATAGC-TGT-----CCC-----	3472
OY	208	IarThrTyrAspTyrArgSer-AspIle-----Trp-----SerLeuGlyIleThr--	222
Db	3471	-----CGAGT-CGACATCCACAGCATGAGAGCAGC-----ACTGGA	3436
OY	223	AlaIleGluMetAla--GluGly--AlaProProLeu-CysAspMetHis--Prom	239
Db	3435	GCCATAG--ATGACCTTAGCC-GCTGCCCTCTCTCTACTGT-----CAGGTGACACG	3385
OY	239	eArg-----Ala-----Leu-----Phe-----L	244
Db	3384	C-AsAGGGCGGTGGGGAGGTGGCAAGACTTGAAGGCCATGAATTTGTGTAGGCTT	3326
OY	244	eulle--ProArgAsnPro--ProProArgLeuLysSerLysTyrSerLysLysPheI	263
Db	3325	TGGG-GGCCCAAGGATAC-ACTCTCAGG-----AGC-----TCTT-----	3292
OY	263	leapPheIleAsp-ThrCys-----IeuIleLysThrTyrLeuSer-----	276
Db	3291	--GAGG--GC-GATGACAG-GAACTTAATTCGCTGTATT--TCAACAACGGTAGTGC	3240
OY	277	Arg-----Pro-----ProThrGlnu--Gln--LeuLeuLysPhe-Pro-Phe--	288
Db	3239	CCGAGCCCTTCATGTGCCCAAGGT-GGTTCAGCCCTGTCTTCTTCTCACTTCGGG	3183
OY	289	--IleArgAspGln-----ProThrGlnu--Arg-GlnValArgIleGlnLeuLysA	304
Db	3182	TCATTTG--TG-CAGAAATCTTGTTCCG--GAGCCAGAGCAGTA--ATA-----	3142

Db	181	GACGAGGAGGAAGATCAAAACAGGAGTCAAACTGCTGAAAAAGTACTCTCAACACCCG	240
Oy	247	AACATCGCCACTTACTACGAGCCTTCAACAAGAGCCCCCGGGAACGATGACCG	306
Db	241	AACATCGCCACTTACTACGAGCCTTCAACAAGAGCCCCCGGGAACGATGACCG	300
Oy	307	CTCTGGCTGGTGAATGAGATTCTGTGGTGTGATGATGACCTGATCTGGTAAAGACA	366
Db	301	CTCTGGCTGGTGAATGAGATTCTGTGGTGTGATGATGACCTGATCTGGTAAAGACA	360
Oy	367	AAAGGCAACGCCCTGAAGAGGACTGTATCGCCTTATCTGACGGGAGATCCTCAGGGGT	426
Db	361	AAAGGCAACGCCCTGAAGAGGACTGTATCGCCTTATCTGACGGGAGATCCTCAGGGGT	420
Oy	427	CTGGCCCATCTCCATGCCCCAACAGGTGATCATGACATCAAGGGCAGATGTGCTG	486
Db	421	CTGGCCCATCTCCATGCCCCAACAGGTGATCATGACATCAAGGGCAGATGTGCTG	480
Oy	487	CTGACAGGAATGCTGAGGTCAAGCTAATGGAATTTTGGGGTGAATGCTCAGCTGACCCG	546
Db	481	CTGACAGGAATGCTGAGGTCAAGCTAATGGAATTTTGGGGTGAATGCTCAGCTGACCCG	540
Oy	547	ACCGTGGACACGGAACATTTCAATTGGGACTCCCTACTGGAATGGCTCCAGAGTATC	606
Db	541	ACCGTGGACACGGAACATTTCAATTGGGACTCCCTACTGGAATGGCTCCAGAGTATC	600
Oy	607	GCTGTGATGAAACCTGTATGCCACTATGATTAACAGAGTGATATTGGTCTCTAGA	666
Db	601	GCTGTGATGAAACCTGTATGCCACTATGATTAACAGAGTGATATTGGTCTCTAGA	660
Oy	667	ATCAACGCCATTCGAATGGCAGAGGAGACCCCCCTCTGTGTGACATGCAACCCATGCA	726
Db	661	ATCAACGCCATTCGAATGGCAGAGGAGACCCCCCTCTGTGTGACATGCAACCCATGCA	720
Oy	727	GCCCTCTTCCTCATCTCTCGGAAACCTTCGCGCCAGGCTCAAGTCCAAAGATGGTCTAAG	786
Db	721	GCCCTCTTCCTCATCTCTCGGAAACCTTCGCGCCAGGCTCAAGTCCAAAGATGGTCTAAG	780
Oy	787	AAGTTCATTGACTTCATTGAACATGTCTCAACAATTACCTGAGCCGCCACCCACG	846
Db	781	AAGTTCATTGACTTCATTGAACATGTCTCAACAATTACCTGAGCCGCCACCCACG	840
Oy	847	GAGCAGCTACTGAAGTTTCCCTTCAATCCGGGACACAGCCACAGAGCCGACAGTCCGATC	906
Db	841	GAGCAGCTACTGAAGTTTCCCTTCAATCCGGGACACAGCCACAGAGCCGACAGTCCGATC	900
Oy	907	CAGCTTAAGAACCAATGACCGATCCCGGAAAGAGCGGGGTGAAGAAAGAGAACGAA	966
Db	901	CAGCTTAAGAACCAATGACCGATCCCGGAAAGAGCGGGGTGAAGAAAGAGAACGAA	960
Oy	967	TATGAGTACAGCGGACGAGAGGAGAGATGACAGCCATGAGAGGAAGAGAGCCCAAGC	1026
Db	961	TATGAGTACAGCGGACGAGAGGAGAGATGACAGCCATGAGAGGAAGAGAGCCCAAGC	1020
Oy	1027	TCCATCATGAACGTGCTTGAGAGTGCATCTGAGCCGGAGATTCTTCGGCTCCAGAG	1086
Db	1021	TCCATCATGAACGTGCTTGAGAGTGCATCTGAGCCGGAGATTCTTCGGCTCCAGAG	1080
Oy	1087	GAAAAATAAGACAATCAGAGGCTTTAAACAGGACGACGCTGACAGACACACACACAG	1146
Db	1081	GAAAAATAAGACAATCAGAGGCTTTAAACAGGACGACGCTGACAGACACACACACAG	1140
Oy	1147	CGAGACCCCGGACACATCAAAACCTGTGCAACAGCGGACAGCGGCGCATAGAGAG	1206
Db	1141	CGAGACCCCGGACACATCAAAACCTGTGCAACAGCGGACAGCGGCGCATAGAGAG	1200
Oy	1207	CAGAAAGAGAGCGGCGCGGTGAGAGCAACAGCGGCGGAGCGGAGCAGCTGAG	1266
Db	1201	CAGAAAGAGAGCGGCGCGGTGAGAGCAACAGCGGCGGAGCGGAGCAGCTGAG	1260
Oy	1267	CTGACAGGAAGAGACACAGCGCGGCTTGAGAGCATGACAGCTCTTCGGCGGGAAGAG	1326
Db	1261	CTGACAGGAAGAGACACAGCGCGGCTTGAGAGCATGACAGCTCTTCGGCGGGAAGAG	1320

QY	1327	GAGGGGCGGCGAGCGCGGAGCGTGAAGAGATTAACAAGGGGAAAGCAAGCGCTGGAGGAGCAACGG	1386
Db	1321	GAGCGGCGGCGAGCGCGAGCGGAGAGAAATTAACAAGCGGAAAGCAAGCTGGAGAGCAACGG	1380
QY	1387	CAGTCAGAAAGCTCTCCAGAGGCAAGCTCACAGGAGCATGCTCACTCAAGTCCCTGAC	1446
Db	1381	CAGTCAGAAAGCTCTCCAGAGGCAAGCTCACAGGAGCATGCTCACTCAAGTCCCTGAC	1440
QY	1447	CAGCAGCAACAGCAGCAGCAAGCTTACAGAAACAGCAGCAGCAGCAAGCTTCTGCTGGGAC	1506
Db	1441	CAGCAGCAACAGCAGCAGCAAGCTTACAGAAACAGCAGCAGCAGCAAGCTTCTGCTGGGAC	1500
QY	1507	AGGAAGCCCTCTGATCACTTAATGCTGGGGGATGAATCCCGCTGACAAACCAAGCTTGGGCC	1566
Db	1501	AGGAAGCCCTCTGATCACTTAATGCTGGGGGATGAATCCCGCTGACAAACCAAGCTTGGGCC	1560
QY	1567	CGAGAGGTAGAAGAGAGAAACAAGGATTAACAAGAGAGAGAATCTCCCTTGGCCAAAGC	1626
Db	1561	CGAGAGGTAGAAGAGAGAAACAAGGATTAACAAGAGAGAGAATCTCCCTTGGCCAAAGC	1620
QY	1627	AAGCCAGGCAACAGCGGGGCTGAGCCGCCCATCCCGAGGCTTCCCGAGGGCCCCCAGGA	1686
Db	1621	AAGCCAGGCAACAGCGGGGCTGAGCCGCCCATCCCGAGGCTTCCCGAGGGCCCCCAGGA	1680
QY	1687	CCCCCTTTCCCAAGATCTCTCTATGCAAGGCGGCTGAGCCCGCCAGAGGGAACGCAACA--	1744
Db	1681	CCCCCTTTCCCAAGATCTCTCTATGCAAGGCGGCTGAGCCCGCCAGAGGGAACGCAACAAG	1740
QY	1745	-----AG	1746
Db	1741	AGCCTGGTGGCAACCGGGTCCACTGAAGCATATGCAAGCATCTGATCCCGATCCGAG	1800
QY	1747	TCCTCTGAGAGACAGCCCAACCCGAAACCTGAGCTGCTTCCAGCTTCCATGAACCCCGAC	1806
Db	1801	TCCTCTGAGAGACAGCCCAACCCGAAACCTGAGCTGCTTCCAGCTTCCATGAACCCCGAC	1860
QY	1807	CTGCGCATCCCGGACCCCATCTGCGCAGCCCACTGTCGCCGAGAGCTGTATCTCCGCAAGT	1866
Db	1861	CTGCGCATCCCGGACCCCATCTGCGCAGCCCACTGTCGCCGAGAGCTGTATCTCCGCAAGT	1920
QY	1867	TCGACACCCCACTCTTGAAGACCTGAGGCGCCGACCCGAAATCCCGAGCTGGGTCCGCGCA	1926
Db	1921	TCGACACCCCACTCTTGAAGACCTGAGGCGCCGACCCGAAATCCCGAGCTGGGTCCGCGCA	1980
QY	1927	GATTAACGAGGCGCCCAACCAAGTGTCTCAGAGAGCTCATCTATCGCACATGCGCTTTAAC	1986
Db	1981	GATTAACGAGGCGCCCAACCAAGTGTCTCAGAGAGCTCATCTATCGCACATGCGCTTTAAC	2040
QY	1987	ACCAAGTGGGGCGGAGGGGTCCCGGCAAGCCCAAGCAAGTCCGTGCGAGACCTCGCAGCAAC	2046
Db	2041	ACCAAGTGGGGCGGAGGGGTCCCGGCAAGCCCAAGCAAGTCCGTGCGC-----	2085
QY	2047	TCGCGCTGGCAAACTCTATCTGCAAAAGGCGGAGCAAGCGGGGCAACCCCAAAGCTTCAAGG	2106
Db	2086	-----	2085
QY	2107	CCCCCTGTGACGCCCCGCGGCGCCCAAGCCTCTAGTAACCCCGACCTCAGAGGAGAGC	2166
Db	2086	-----AGTAACCCCGACCTCAGAGGAGAGC	2109
QY	2167	GACCTGGCTGGAGAACGCTCGAGCAAGCGTCTTTCAGACCTTCAACCGGCAACTTCCCGCAG	2226
Db	2110	GACCTGGCTGGAGAACGCTCGAGCAAGCGTCTTTCAGACCTTCAACCGGCAACTTCCCGCAG	2169
QY	2227	GCTGGCTCACTGAGCGGAACCGCGCTGGAG-G-CTCTCTCAAA-CTTGAACAAGTCCCTTG	2284
Db	2170	GCTGGCTCACTGAGCGGAACCGCGCTGGAGTTC-CTCTCAAAAC--GGAACAAGTCCCTTG	2227
QY	2285	TGCTCTCCCTCGGGAATAAAGCCAAAGCCGACGACCAACGCTCAACGGCGCAGGCGCGCGCG	2344
Db	2228	TGCTCTCCCTCGGGAATAAAGCCAAAGCCGACGACCAACGCTCAACGGCGCAGGCGCGCGCG	2287


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2288 CAGACTTGTGTGTAAGAGAGCGGACTGTGACGAGGCGCCCTCGGCTCCCAAGAGG 2347
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2348 CCATGGAATCTCTGTGTGTGACGAGAGGTGGAAGCACTGAGAGAGAGAG 2407
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2408 GCGAAGGCGGCGGACGAGAGGAGAGAGTACCCCTGGGGGCGGAGAGAGAG 2467
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2828 CTGGGCTGTGTAAGAGCGCCCTGGGAGAGTGTGTAAGTGTGTGATCTA 2887
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3005 CCGAAGACAGCAATGAGTCAACAATGATGTGTGACGAGAGAGAGAGAG 3064
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3065 TGAATGTGTGTAAGAGCGCCCTGGGAGAGTGTGTAAGTGTGTGATCTA 3124
3008 TGAATGTGTGTAAGAGCGCCCTGGGAGAGTGTGTAAGTGTGTGATCTA 3067
3125 TCCAGCAGATGATGTGTGAGAGGCTCAACCTGTCTATCACTCAAGAGAGAG 3184
3068 TCCAGCAGATGATGTGTGAGAGGCTCAACCTGTCTATCACTCAAGAGAGAG 3127
3185 ACACACTGCGGCGGTAATCACTGTGTGTGACGAGAGAGAGAGAGAGAG 3244
3128 ACACACTGCGGCGGTAATCACTGTGTGTGACGAGAGAGAGAGAGAGAG 3187
3245 AAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3304
3188 AAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3247
3305 GTGTGTGTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3364
3248 GTGTGTGTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3307
3365 GTGTGTGTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3424
3308 GTGTGTGTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3367
3425 TCCCCCAGCGGCGGCTGTGTGTGACGAGAGAGAGAGAGAGAGAGAGAG 3484

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Db 3368 TCCCCCAGCGGCGGCTGTGTGTGACGAGAGAGAGAGAGAGAGAGAGAG 3427
Oy 3485 TGTATGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3544
Db 3428 TGTATGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3487
Oy 3545 TGTATGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3604
Db 3488 TGTATGCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3547
Oy 3605 ACACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3664
Db 3548 ACACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3607
Oy 3665 ACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3724
Db 3608 ACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3667
Oy 3725 ACATGTGTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3784
Db 3668 ACATGTGTCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3727
Oy 3785 ACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3844
Db 3728 ACAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3787
Oy 3845 GTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3904
Db 3788 GTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3847
Oy 3905 ACTTCATGACTGTGAACCGTGAACGATCAATGATGATGATGATGATGAT 3945
Db 3848 ACTTCATGACTGTGAACCGTGAACGATCAATGATGATGATGATGATGAT 3888

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RESULT 2

ab035698/c
TOIG of: ab035698 check: 9874 From: 1 to: 3888

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LOCUS AB035698 3888 bp mRNA linear PRI 18-APR-2000
DEFINITION Homo sapiens mRNA for Mieshaen/NIR-related kinase MINK-1, complete cds.
ACCESSION AB035698
VERSION AB035698.1 GI:6970477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Gileb)
AUTHORS Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K.,
Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M.,
Matsumoto, K., Ninomiya-Tsuji, J. and Kusumi, A.
TITLE Molecular cloning of MINK, a novel member of mammalian GCK family
kinases, which is up-regulated during postnatal mouse cerebral
development
JOURNAL FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE 20175403
PubMed 10708748
REFERENCE
2 (bases 1 to 3888)
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DIRECT SUBMISSION
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2752 -C---AAACAT-----CGTGAAC---GA-GCTCTT-----GC-CAG-G-G-GCCT 2720

1136 --AGCAGCAG-C-CAAGGAGACCCC-GAG--G-CACACA-T-CMAACA-CCTGCTGCACC- 1183

2719 TTA-C-C-CAAGCCCA-CGAGA---CTG-GTATGTCAC-CACTGC---CATCTT-T-----CG 2678

1184 AACGG---GCAGC---GGC-----GCATAG---AGAGACGAAG-GAG-GAGC-GGCGCC 1226

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1227 CGTGGAGAGCAACA-G-C-GGCGGAGAGC---G-G-AGCAGCGAA--GGTG-CAG--- 1272

2631 C-TGGA-----C-CACGTACAGC---AG-GTTTGTGTACC-C--ATTGCTGTACGAT 2588

1273 G-AG-AAGAG---CAG-----CAGCGCGC---GCTGAGG-A-CATCAG-GCTCT 1313

2587 GCAGCA-G-GTTTC-GCTCTTCTTACAG-GG-GTGGCTGTGA-CCACCATG--GTGC-C- 2539

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OY	2061	C---TA---T-CTGCA-A-GGC---G-GGACAGC--GG-G-GCACCCAAAGCT	2100
Db	1793	CGGGATACAGGTGCTGC-ATATGACTTCAGTGG--GA-CCGGAGTGG--CCA-----	1748
OY	2101	CCAGGGCCCC-C-TGCT-CAG--CCC-CCT-GGGCCGC-CCAA-C-GCTTATGAACC	2156
Db	1747	CCAGG---CTCTTG-TGC-GATCCCTCTGGG--GCTCC-ACCAGGCTCT-G-----	1705
OY	2151	CGACCTCAGAGAGACACCCCTGGCTGGG-AACGCTGCAGAGGCTCTTCAGAGCTTC	2209
Db	1704	C-A--T-AGAGAGAG-----T-CTGGAAA-----GG--G-GTCTT--G-----	1676
OY	2210	ACG-GGCACCTCCCCCAGGCTGGCTCA--CTGAGCGGAACCGCGTGGAGCTTC--C	2262
Db	1675	--GGGGC-CCT-----GG--GG--AGGCTGG-G-GGA-TG-G-GGG-G-CTCAGGC	1638
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